

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/089,057A

Source: IFW16

Date Processed by STIC: 10/18/04

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/089,057A

DATE: 10/18/2004
 TIME: 09:38:04

Input Set : A:\PTO.FG.txt
 Output Set: N:\CRF4\10182004\J089057A.raw

3 <110> APPLICANT: HIRANO, SEIKO
 4 KIMURA, EIICHIRO
 5 OSUMI, TSUYOSHI
 6 MATSUI, KAZUHIKO
 7 KAWAHARA, YOSHIO
 8 NONAKA, GEN
 9 MATSUZAKI, YUMI
 10 AKIYOSHI, NAOKI
 11 NAKAMURA, KANAE
 12 KURAHASHI, OSAMU
 13 NAKAMATSU, TSUYOSHI
 14 SUGIMOTO, SHINICHI
 16 <120> TITLE OF INVENTION: GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY
 17 DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA
 W--> 18 <130> FILE REFERENCE: 221519US0PCT
 20 <140> CURRENT APPLICATION NUMBER: 10/089,057A
 21 <141> CURRENT FILING DATE: 2002-04-03
 23 <150> PRIOR APPLICATION NUMBER: PCT/JP00/06913
 24 <151> PRIOR FILING DATE: 2000-10-04
 26 <150> PRIOR APPLICATION NUMBER: JP 11-282716
 27 <151> PRIOR FILING DATE: 1999-10-04
 29 <150> PRIOR APPLICATION NUMBER: JP 11-311147
 30 <151> PRIOR FILING DATE: 1999-11-01
 32 <150> PRIOR APPLICATION NUMBER: JP 2000-120687
 33 <151> PRIOR FILING DATE: 2000-04-21
 35 <160> NUMBER OF SEQ ID NOS: 108
 37 <170> SOFTWARE: PatentIn version 3.1
 39 <210> SEQ ID NO: 1
 40 <211> LENGTH: 1980
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Corynebacterium thermoaminogenes
 44 <220> FEATURE:
 45 <221> NAME/KEY: CDS
 46 <222> LOCATION: (577)..(1869)
 48 <400> SEQUENCE: 1
 49 tgcattccac cgacggtcac gcgttccggc ttgtcagcggt cgtcaatctg ctgatggttc 60
 50 atgaaagact ccttcgaagc aagagatcggt gtgtgtcggt gcacccatcg gggaaagccc 120
 51 tcgctgcgcc ccaggggggag ctggcgatgt gaccagggtta agtgataacc atcaccttgc 180
 52 caatgggttt gcgaacttta ccgtgacgct acccccgctt ttgtttgatc acaccagctc 240
 53 gaaggctgtc gctttccga agatgcacgt gaagtggcaa atccttgcca cccgagggttt 300
 54 tccccgttaca aacgtacttag tgatgaggat cacggggAAC attgtggaga ttgcactttg 360
 55 caatatttgc aaaagggggtg actaccccccg cgaaaaactt aaaaacccaa atccgttgac 420
 56 ggacccatgc ccgtatgaa aatgtgtgaa gcacgccacc ggaacacagg ttgtggatca 480

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57	ctcaccatga	tgtggggat	tcgcatacaca	cagtgtgcag	ggccgcaccc	ctaccgaatg	540		
58	cgccttacag	cagcaccaag	aagaagtgc	tcttag	atg tca aac	gtt gga acg	594		
59					Met Ser Asn Val	Gly Thr			
60					1	5			
61	cca cgt acc	gca cag	gaa atc	cag cag	gat tgg	gac acc aac	cca cgc	642	
62	Pro Arg Thr	Ala Gln	Glu Ile	Gln Gln	Asp Trp	Asp Thr Asn	Pro Arg		
63	10	15	20						
64	tgg aac gga atc	acc cgc	gac tac	acc gct	gag cag	gta gct	gag ctc	690	
65	Trp Asn Gly	Ile Thr Arg	Asp Tyr	Thr Ala	Glu Gln	Val Ala	Glu Leu		
66	25	30	35						
67	cag ggc agc	gtc gtc	gag gag	cac acc	ctc gca	aag cgc	ggc gcc gag	738	
68	Gln Gly Ser	Val Val	Glu Glu	His Thr	Leu Ala	Lys Arg	Gly Ala Glu		
69	40	45	50						
70	atc ctg tgg	gat gca	gtt tcc	gca gag	ggc gac	gac tac	atc aac	gca	786
71	Ile Leu Trp	Asp Ala Val	Ser Ala	Glu Gly	Asp Asp	Tyr Ile	Asn Ala		
72	55	60	65	70					
73	ctg ggc gcc	ctt acc	ggt aac	cag gct	gtc cag	cag gtc	cgt gcc ggc	834	
74	Leu Gly Ala	Leu Thr Gly	Asn Gln	Ala Val	Gln Gln	Val Arg	Ala Gly		
75	75	80	85						
76	ctg aag gct	gtc tac	ctc tcc	ggc tgg	cag gtc	gca ggt	gac gcc aac	882	
77	Leu Lys Ala	Val Tyr Leu	Ser Gly	Trp Gln	Val Ala	Gly Asp	Ala Asn		
78	90	95	100						
79	ctc gcc ggt	cac acc	tac ccc	gac cag	tcc ctg	tac ccg	gcg aac	930	
80	Leu Ala Gly	His Thr Tyr	Pro Asp Gln	Ser Leu	Tyr Pro	Ala Asn	Ser		
81	105	110	115						
82	gtc ccg aac	gtt gtc	cgt cgc	atc aac	aac gca	ctg ctg	cgc gcc gat	978	
83	Val Pro Asn	Val Val	Arg Arg	Ile Asn	Asn Ala	Leu Leu	Arg Ala Asp		
84	120	125	130						
85	gag atc	gca cgc	gtc gag	ggt gac	acc tcc	gtc gac	aac tgg ctc gtc	1026	
86	Glu Ile Ala	Arg Val	Glu Gly	Asp Thr	Ser Val	Asp Asn	Trp Leu Val		
87	135	140	145	150					
88	ccg atc	gtc gcc	gac ggc	gag gcc	ggc ttc	ggt ggc	gcc ctc aac gtc	1074	
89	Pro Ile Val	Ala Asp	Gly Glu	Ala Gly	Phe Gly	Gly Ala	Leu Asn Val		
90	155	160	165						
91	tac gag	ctc cag	aag ggc	atg atc	acc gct	ggt gcc gca	ggc acc cac	1122	
92	Tyr Glu Leu	Gln Lys Gly	Met Ile	Thr Ala	Gly Ala	Ala Gly	Thr His		
93	170	175	180						
94	tgg gag	aat ctc	gat ctc	gct tcc	gag aag	aag tgt	ggc cac ctc ggt ggc	1170	
95	Trp Glu Asp	Gln Leu Ala	Ser Glu	Lys Lys	Cys Gly	His Leu	Gly Gly		
96	185	190	195						
97	aag gtc	ctc atc	ccg acc	cag cag	cac atc	ccg acc	ctg aac tcc gcc	1218	
98	Lys Val Leu	Ile Pro	Thr Gln	Gln His	Ile Arg	Thr Leu	Asn Ser Ala		
99	200	205	210						
100	ccg ctg	gca gct	gac gtg	gcc aac	acc ccg	acc gtc	atc gcc cgc	1266	
101	Arg Leu Ala	Ala Asp	Val Ala	Asn Thr	Pro Thr	Val Val	Ile Ala Arg		
102	215	220	225	230					
103	acc gac	gca gag	gcc acc	ctg atc	acc tct	gat gtt	gat gag cgc	1314	
104	Thr Asp Ala	Glu Ala	Ala Thr	Leu Ile	Thr Ser	Asp Val	Asp Glu Arg		
105	235	240	245						

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106 gac cgc cca ttc atc acc ggc gag cgc acc gcc gag ggc tac tac cac 1362
 107 Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr His
 108 250 255 260
 109 gtc aag ccg ggt ctc gag ccc tgc atc gca cgt gcg aag tcc tac gct 1410
 110 Val Lys Pro Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr Ala
 111 265 270 275
 112 ccc tac gca gac atg atc tgg atg gag acc ggc acc cct gac ctc gag 1458
 113 Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu Glu
 114 280 285 290
 115 ctg gcc aag aag ttc gcc gag ggc gtc cgc agc gag ttc ccg gac cag 1506
 116 Leu Ala Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp Gln
 117 295 300 305 310
 118 ctg ctg tcc tac aac tgc tcc ccg tcc aac tgg tct gca cac ctc 1554
 119 Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His Leu
 120 315 320 325
 121 gag gcc gac gag atc gct aag ttc cag aag gaa ctg ggt gcc atg ggc 1602
 122 Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met Gly
 123 330 335 340
 124 ttc aag ttc cag ttc atc acc ctg gct ggc ttc cac tcc ctc aac tac 1650
 125 Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn Tyr
 126 345 350 355
 127 ggt atg ttc gac ctg gct tac ggc tac gcc cgt gaa ggc atg ccc gcc 1698
 128 Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Pro Ala
 129 360 365 370
 130 ttc gtc gac ctg cag aac cgt gag ttc aag gca gct gag gag cgc ggc 1746
 131 Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg Gly
 132 375 380 385 390
 133 ttc acc gcc gtc aag cac cag cgt gag gtc ggc gcc ggc tac ttc gac 1794
 134 Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe Asp
 135 395 400 405
 136 acc atc gcc acc acc gtt gac ccg aac tcc tcc acc acc gcg ctg aag 1842
 137 Thr Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu Lys
 138 410 415 420
 139 ggt tcc acc gag gaa tgc cag ttc cac taggaaccac ctgtatgcgg 1889
 140 Gly Ser Thr Glu Glu Cys Gln Phe His
 141 425 430
 142 gccgtatggc ctgacggcac cgccccctccc tttgcactcc agtactcctt tgtgcacatc 1949
 143 ggccatctcc acaccgcgcg ccccgccacc t 1980
 145 <210> SEQ ID NO: 2
 146 <211> LENGTH: 431
 147 <212> TYPE: PRT
 148 <213> ORGANISM: Corynebacterium thermoaminogenes
 150 <400> SEQUENCE: 2
 151 Met Ser Asn Val Gly Thr Pro Arg Thr Ala Gln Glu Ile Gln Asp
 152 1 5 10 15
 153 Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
 154 20 25 30
 155 Glu Gln Val Ala Glu Leu Gln Gly Ser Val Val Glu Glu His Thr Leu
 156 35 40 45

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157 Ala Lys Arg Gly Ala Glu Ile Leu Trp Asp Ala Val Ser Ala Glu Gly
 158 50 55 60
 159 Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 160 65 70 75 80
 161 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 162 85 90 95
 163 Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
 164 100 105 110
 165 Leu Tyr Pro Ala Asn Ser Val Pro Asn Val Val Arg Arg Ile Asn Asn
 166 115 120 125
 167 Ala Leu Leu Arg Ala Asp Glu Ile Ala Arg Val Glu Gly Asp Thr Ser
 168 130 135 140
 169 Val Asp Asn Trp Leu Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 170 145 150 155 160
 171 Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala
 172 165 170 175
 173 Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 174 180 185 190
 175 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 176 195 200 205
 177 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 178 210 215 220
 179 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 180 225 230 235 240
 181 Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr
 182 245 250 255
 183 Ala Glu Gly Tyr Tyr His Val Lys Pro Gly Leu Glu Pro Cys Ile Ala
 184 260 265 270
 185 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 186 275 280 285
 187 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 188 290 295 300
 189 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 190 305 310 315 320
 191 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 192 325 330 335
 193 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 194 340 345 350
 195 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 196 355 360 365
 197 Arg Glu Gly Met Pro Ala Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 198 370 375 380
 199 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
 200 385 390 395 400
 201 Gly Ala Gly Tyr Phe Asp Thr Ile Ala Thr Thr Val Asp Pro Asn Ser
 202 405 410 415
 203 Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Cys Gln Phe His
 204 420 425 430
 206 <210> SEQ ID NO: 3

RAW SEQUENCE LISTING
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Input Set : A:\PTO.FG.txt
 Output Set: N:\CRF4\10182004\J089057A.raw

207 <211> LENGTH: 2381
 208 <212> TYPE: DNA
 209 <213> ORGANISM: Corynebacterium thermoaminogenes
 211 <220> FEATURE:
 212 <221> NAME/KEY: CDS
 213 <222> LOCATION: (577) .. (2349)
 215 <400> SEQUENCE: 3
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 217 cgcacctcaa ccctgccgag gacaccgtgg tgtactgcgc cgtgggtgac cgccgcggccc 120
 218 acacctgggtt cgtgttgaag tacctgctgg gtttgaaaaa cgtccgcaac tatgacgggtt 180
 219 cctggccgaa gtggggcaac atggtgcgca tgcccatcgt ccaggggtat gagccggct 240
 220 cactctagtc acccccgggtt cacccctg gtcacccccc tacccctccc ggtacacccc 300
 221 ggggacgggg tttttttttt atctccctg catgtggaca ccggaaaact ttgcctggaa 360
 222 aatgaccata cagtaccgtt atgcgggtat gttAACGCGG tcacagggtt caccagaatc 420
 223 cggatcgctt aacccttta gcgggattcg ctAAAAGATC accggatgtt tttttttttt 480
 224 taatgtgtat cgcaggggca ctgtcataacg ctgtcatgtt gtaatgttac agtgcgggtgc 540
 225 tctgtcgtt agaaaatcaa aaccaggagg gtttttta gtttttta gtttttta gtttttta 594
 226 Val Ser Val Glu Thr Arg
 227 1 5
 228 aag atc acc aag gta ctt gtc gcc aac cgt ggt gaa atc gca atc cgt 642
 229 Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile Arg
 230 10 15 20
 231 gtt ttc cgc gca gca cgg gat gaa ggc atc gcc tct gtc gcc gtc tac 690
 232 Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr
 233 25 30 35
 234 gcg gag ccg gac gca gat gcc cct ttc gtc gag tat gcc gat gag gcc 738
 235 Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Glu Tyr Ala Asp Glu Ala
 236 40 45 50
 237 ttc gca ctc ggt ggc cag act tcc gca gag tcc tac ctc gtc att gac 786
 238 Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp
 239 55 60 65 70
 240 aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc 834
 241 Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pro
 242 75 80 85
 243 ggc tac ggc ttc ctc gcc gag aac gcc gat ttc gct gaa gct gtc atc 882
 244 Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
 245 90 95 100
 246 aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc 930
 247 Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
 248 105 110 115
 249 ctc ggt gac aag gtc acc gca cgc cac atc gcc aac aac gcc aac gca 978
 250 Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
 251 120 125 130
 252 ccg atg gca ccc ggc acc aag gag cct gtc aag gac gcc gct gag gtt 1026
 253 Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu Val
 254 135 140 145 150
 255 gtc gcc ttc gcc gag gag ttc ggt ctc ccc atc gcc atc aag gct gcc 1074
 256 Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala Ala
 257 155 160 165

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\PTO.FG.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 3
Seq#:46; N Pos. 18
Seq#:55; N Pos. 3,6,9
Seq#:56; N Pos. 3,9,18
Seq#:83; N Pos. 9

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10182004\J089057A.raw

:18 M:283 W: Missing Blank Line separator, <130> field identifier
3855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
3871 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
3985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
4011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
4606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0